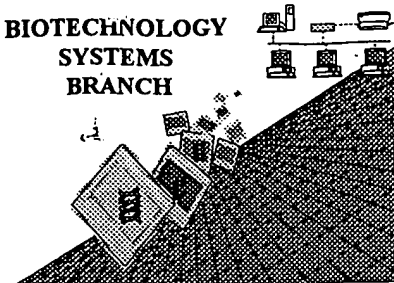


P. Holbrook

## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/646,224

Source: OIPR

Date Processed by STIC: 9/18/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/646,224

DATE: 09/18/2001

TIME: 10:11:16

Input Set : A:\Pg3432.app

Output Set: N:\CRF3\09182001\I646224.raw

4 <110> APPLICANT: Glaxo Wellcome PLC  
 5 Tate, Simon N  
 6 Grose, David T  
 7 Hicks, Caroline A  
 9 <120> TITLE OF INVENTION: Ion Channels  
 11 <130> FILE REFERENCE: PG3432  
 13 <140> CURRENT APPLICATION NUMBER: US/09/646,224  
 14 <141> CURRENT FILING DATE: 2001-08-30  
 16 <150> PRIOR APPLICATION NUMBER: GB 9805793.8  
 17 <151> PRIOR FILING DATE: 1998-03-18  
 19 <160> NUMBER OF SEQ ID NOS: 35  
 21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
 Corrected Diskette Needed

## ERRORED SEQUENCES

500 <210> SEQ ID NO: 2  
 501 <211> LENGTH: 1765  
 502 <212> TYPE: PRT  
 503 <213> ORGANISM: Rattus norvegicus  
 505 <400> SEQUENCE: 2  
 506 Met Glu Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe  
 507 1 5 10 15  
 509 Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Lys Lys Arg Ile Ala  
 510 20 25 30  
 512 Ile Gln Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro  
 513 35 40 45  
 515 Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys  
 516 50 55 60  
 518 Leu Tyr Gly Asp Ile Pro Pro Glu Leu Val Thr Lys Pro Leu Glu Asp  
 519 65 70 75 80  
 521 Leu Asp Pro Tyr Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys  
 522 85 90 95  
 524 Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu  
 525 100 105 110  
 527 Gly Pro Phe Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His  
 528 115 120 125  
 530 Ser Val Phe Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met  
 531 130 135 140  
 533 Phe Met Ala Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu  
 534 145 150 155 160  
 536 Tyr Val Phe Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu  
 537 165 170 175  
 539 Ala Arg Gly Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp  
 540 180 185 190  
 542 Asn Trp Leu Asp Phe Ile Val Ile Gly Thr Ala Ile Ala Thr Cys Phe  
 543 195 200 205

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545 Pro Gly Ser Gln Val Asn Leu Ser Ala Leu Arg Thr Phe Arg Val Phe
546      210      215      220
548 Arg Ala Leu Lys Ala Ile Ser Val Ile Ser Gly Leu Lys Val Ile Val
549 225      230      235      240
551 Gly Ala Leu Leu Arg Ser Val Lys Lys Leu Val Asp Val Met Val Leu
552      245      250      255
554 Thr Leu Phe Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe
555      260      265      270
557 Met Gly Ile Leu Asn Gln Lys Cys Ile Lys His Asn Cys Gly Pro Asn
558      275      280      285
560 Pro Ala Ser Asn Lys Asp Cys Phe Glu Lys Glu Lys Asp Ser Glu Asp
561      290      295      300
563 Phe Ile Met Cys Gly Thr Trp Leu Gly Ser Arg Pro Cys Pro Asn Gly
564 305      310      315      320
566 Ser Thr Cys Asp Lys Thr Thr Leu Asn Pro Asp Asn Asn Tyr Thr Lys
567      325      330      335
569 Phe Asp Asn Phe Gly Trp Ser Phe Leu Ala Met Phe Arg Val Met Thr
570      340      345      350
572 Gln Asp Ser Trp Glu Arg Leu Tyr Arg Gln Ile Leu Arg Thr Ser Gly
573      355      360      365
575 Ile Tyr Phe Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe
576      370      375      380
578 Tyr Leu Leu Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu
579 385      390      395      400
581 Gln Asn Arg Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe
582      405      410      415
584 Gln Glu Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala
585      420      425      430
587 Met Gly Ile Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe
588      435      440      445
590 Ser Pro Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe
591      450      455      460
593 Phe Met Arg Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu
594 465      470      475      480
596 Asp Asp Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu
597      485      490      495
599 Ser Gln Asn Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu
600      500      505      510
602 His Arg Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Ile
603      515      520      525
605 Gln Glu Gln Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn
606      530      535      540
608 Leu Ala Ser Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys
609 545      550      555      560
611 Ile Lys Lys Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu
612      565      570      575
614 Ala Ile Thr Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu
615      580      585      590
617 His His Asn Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn

```

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618	595	600	605
620 Trp Val Phe Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile			
621 610	615	620	
623 Ala Leu Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp			
624 625	630	635	640
626 Ser Ile Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu			
627 645	650	655	
629 Ser Asp Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val			
630 660	665	670	
632 Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile			
633 675	680	685	
635 Ile Gly His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr			
636 690	695	700	
638 Ile Val Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr			
639 705	710	715	720
641 Lys Phe Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg			
642 725	730	735	
644 Trp His Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile			
645 740	745	750	
647 Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met			
648 755	760	765	
650 Asp Gly Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile			
651 770	775	780	
653 Gly Lys Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser			
654 785	790	795	800
656 Phe Ser Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys			
657 805	810	815	
659 Thr Lys Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe			
660 820	825	830	
662 Met Leu His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys			
663 835	840	845	
665 Asn Ser Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn			
666 850	855	860	
668 Lys Asp Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr			
669 865	870	875	880
671 Asp Met Ala Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu			
672 885	890	895	
674 Ala Glu Val Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu			
675 900	905	910	
677 Pro Thr Ser Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro			
678 915	920	925	
680 Glu Thr Lys Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu			
681 930	935	940	
683 Val Phe Ser Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys			
684 945	950	955	960
686 Lys Ser Asp Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu			
687 965	970	975	
689 Asn Asp Ile Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln			
690 980	985	990	

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Input Set : A:\Pg3432.app

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```

692 Pro Asp Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His
693          995          1000          1005
695 Lys Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg
696    1010          1015          1020
698 Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile
E--> 699 1025 1025          1030          1035          1040
701 Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val
702          1045          1050          1055
704 Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu Arg Cys Thr Asp
705          1060          1065          1070
707 Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met Ile Leu Lys Trp Val
708    1075          1080          1085
710 Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser Ala Trp Cys Trp Leu Asp
711    1090          1095          1100
713 Phe Leu Ile Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser
E--> 714 105 1105          1110          1115          1120
716 Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu
717          1125          1130          1135
719 Ser Gln Phe Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala
720          1140          1145          1150
722 Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu
723    1155          1160          1165
725 Val Phe Cys Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg
726    1170          1175          1180
728 Cys Ile Asn Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val
E--> 729 185 1185          1190          1195          1200
731 Pro Asn Arg Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro
732          1205          1210          1215
734 Gln Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln
735    1220          1225          1230
737 Val Ala Thr Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp
738    1235          1240          1245
740 Ser Arg Glu Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala
741    1250          1255          1260
743 Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu
E--> 744 265 1265          1270          1275          1280
746 Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Gln Gln Gln Lys
747          1285          1290          1295
749 Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr
750    1300          1305          1310
752 Tyr Asn Ala Met Lys Lys Leu Gly Thr Lys Lys Pro Gln Lys Pro Ile
753    1315          1320          1325
755 Pro Arg Pro Leu Asn Lys Cys Gln Ala Phe Val Phe Asp Leu Val Thr
756    1330          1335          1340
758 Ser Gln Val Phe Asp Val Ile Ile Leu Gly Leu Ile Val Leu Asn Met
E--> 759 345 1345          1350          1355          1360
761 Ile Ile Met Met Ala Glu Ser Ala Asp Gln Pro Lys Asp Val Lys Lys
762          1365          1370          1375
764 Thr Phe Asp Ile Leu Asn Ile Ala Phe Val Val Ile Phe Thr Ile Glu

```

When  
numbering  
first amino  
acid on a  
line, begin  
number directly  
under first  
letter of amino  
acid

e.g. Lys  
1025

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```

765          1380          1385          1390
767 Cys Leu Ile Lys Val Phe Ala Leu Arg Gln His Tyr Phe Thr Asn Gly
768          1395          1400          1405
770 Trp Asn Leu Phe Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr
771          1410          1415          1420
773 Leu Val Ser Arg Leu Glu Asp Ser Asp Ile Ser Phe Pro Pro Thr Leu
E--> 774 425          1430          1435          1440
776 Phe Arg Val Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val
777          1445          1450          1455
779 Arg Ala Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser
780          1460          1465          1470
782 Leu Pro Ser Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe
783          1475          1480          1485
785 Ile Tyr Ala Ile Phe Gly Met Ser Trp Phe Ser Lys Val Lys Lys Gly
786          1490          1495          1500
788 Ser Gly Ile Asp Asp Ile Phe Asn Phe Glu Thr Phe Thr Gly Ser Met
E--> 789 505          1510          1515          1520
791 Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp Asp Thr Leu Leu
792          1525          1530          1535
794 Asn Pro Met Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp
795          1540          1545          1550
797 Ser Cys Gln Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile
798          1555          1560          1565
800 Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
801          1570          1575          1580
803 Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu
E--> 804 585          1590          1595          1600
806 Asp Asp Phe Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu
807          1605          1610          1615
809 Ala Ser Gln Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala
810          1620          1625          1630
812 Leu Pro Glu Pro Leu Arg Val Ala Lys Pro Asn Lys Phe Gln Phe Leu
813          1635          1640          1645
815 Val Met Asp Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp
816          1650          1655          1660
818 Val Leu Phe Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu
E--> 819 665          1670          1675          1680
821 Asp Thr Met Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro
822          1685          1690          1695
824 Phe Lys Lys Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu
825          1700          1705          1710
827 Glu Glu Gln Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met
828          1715          1720          1725
830 Glu Lys Met Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser Ser His
831          1730          1735          1740
833 Glu Val Phe Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala Lys Val
E--> 834 745          1750          1755          1760
836 Lys Val His Asn Asp
837          1765

```

*same  
err*

VERIFICATION SUMMARY

DATE: 09/18/2001

PATENT APPLICATION: US/09/646,224

TIME: 10:11:17

Input Set : A:\Pg3432.app

Output Set: N:\CRF3\09182001\I646224.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:699 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2

M:332 Repeated in SeqNo=2